IN THE CLAIMS:

1-24. (Previously Canceled)

25. (Presently Amended) A method of detecting a mutation in a target nucleic acid sequence *versus* a known sequence comprising:

a) screening the target sequence by exposing the target sequence to at least one known core sequence probe;

b) determining the binding affinity of the target sequence to the at least one known core sequence probe;

c) determining the binding affinity of the target sequence to at least one probe comprising a single nucleotide variation of the at least one known core sequence probe; and

[~~c~~)] **d)** comparing the binding affinity determined in step b) to the binding [~~affinity~~] **affinity determined in step c** [~~for the same at least one known core sequence probe bound to the known sequence~~];

thereby detecting a mutation in a target nucleic acid sequence *versus* a known sequence.

26. (Previously Presented) A method of claim 25, wherein the at least one known core sequence probe is an array of known core sequence probes.

27. (Previously Presented) A method of claim 25 further comprising before step a), identifying one or more core sequences which are present within the known sequence and would be expected to have high affinity to the target sequence if the target sequence does not contain a mutation.

28. (Presently Presented) A method of claim 25, wherein the binding affinity to the known core sequence probe is plotted as affinity *versus* mismatch position, and normalized to the affinity of a perfect complement of the known core sequence probe.

29. (Previously Presented) A method of claim 28, further comprising determining that the target sequence comprises a mutation versus the known sequence if the pattern formed by the normalized affinity plot of the target sequence does not match the pattern formed by an affinity plot of the perfect complement.

30. (Presently Presented) A method of claim 25, further comprising determining if the binding affinity of the target sequence to the at least one known core sequence probe is weaker than the binding affinity of the known sequence to the at least one known core sequence probe.

31. (Previously Presented) A method of claim 25, wherein the at least one probe is between about 5 and 100 bases in length.

32. (Previously Presented) A method of claim 31, wherein the at least one probe is between about 5 and 50 bases in length.

33. (Previously Presented) A method of claim 32, wherein the at least one probe is between about 8 and 30 bases in length.

34. (Previously Presented) A method of claim 33, wherein the at least one probe is between about 8 and 15 bases in length.

35. (Previously Presented) A method of claim 25, wherein the mutation in the target sequence is indicative of a genetic disease.

36. (Previously Presented) A method of claim 35, wherein the genetic disease is sickle cell anemia.

37. (Previously Presented) A method of claim 35, wherein the genetic disease is cystic fibrosis.

38. (Previously Presented) A method of claim 35, wherein the genetic disease is associated with a P-53 mutation.

39. (Previously Presented) A method of claim 25, wherein the mutation in the target sequence is indicative of a genetic predisposition.

40. (Previously Presented) A method of claim 39, wherein the genetic predisposition is associated with a particular HLA Class I or HLA Class II gene.

41. (Previously Presented) A method of claim 39, wherein the HLA Class II gene is selected from the group consisting of DP, DQ and DR beta.

42. (Previously Presented) A method of claim 25, wherein detecting a mutation in the target sequence is comprised in a genetic evaluation.

43. (Previously Presented) A method of claim 42, wherein the genetic evaluation is a forensics evaluation.

44. (Previously Presented) The method of claim 25, wherein the binding affinity in step b) and c) is absolute binding affinity.

Please add the following new claim:

45. (New) A method of claim 25, wherein said at least one probe comprising a variation of the at least one known core sequence probe is made by substituting A, C, T, U or G at each position of the at least one known core sequence probe.